

FIGURE 1

[illegible]

965	970	975	980	985	990	995	1000	1005	1010	1015	1020	1025	1030	1035	1040											
TAT	CTC	ACC	TTC	ATC	CCT	TCT	GAT	GAC	ATT	TAT	GAC	TGC	AAG	GTC	GAG	CAC	TGG	GGC	CTG	GAG	CCG	GTT	CTG			
ATA	GAG	TGG	AAG	TAG	CGA	AGA	CTA	CTA	CTG	TAA	ATA	CTG	ACG	TTC	CAC	CTC	GAC	CCG	GAC	CTC	CTC	GGC	CAA	GAC		
Tyr	Leu	Thr	Phe	Ile	Pro	Ser	Asp	Asp	Ile	Tyr	Asp	Cys	Lys	Val	Glu	Ile	Trp	Gly	Leu	Glu	Glu	Pro	Val	Leu		
1045	1050	1055	1060	1065	1070	1075	1080	1085	1090	1095	1100	1105	1110	1115	1120											
AAA	CAC	TGG	GAA	CCT	GAG	ATT	CCA	CCC	ATG	TCA	GAG	CTG	ACA	GAA	ACT	GGA	GGT	GGA	TCC	ACT	ACA	GGT	CCA			
Tyr	Glu	ACC	CTT	GGG	CTC	TAA	GGT	CCG	GGG	TAC	ACT	CTC	GAC	TGT	CTT	TGA	CCT	CCA	CCT	CTT	TGA	TGT	CGA	GGT		
Lys	Ile	Trp	Glu	Pro	Glu	Ile	Pro	Ala	Pro	Met	Ser	Glu	Leu	Thr	Glu	Thr	Gly	Gly	Gly	Ser	Thr	Thr	Ala	Pro		
1125	1130	1135	1140	1145	1150	1155	1160	1165	1170	1175	1180	1185	1190	1195												
TCA	GCT	CAG	CTC	GAA	AAA	GAG	CTC	CAG	CCC	CTG	GAG	AAA	GAT	GAA	ACT	GGA	GGT	GGA	TCC	ACT	ACA	GGT	CCA			
Arg	CGA	GTC	GAG	CTT	TTC	CTC	GAG	CTC	TTC	CTT	TTC	CTT	GTC	GAC	CTT	ACC	CTC	ACC	CTC	ACC	GTT	CTT	GAC	CTT		
Ser	Ala	Gln	Leu	Glu	Lys	Glu	Gln	Ala	Lys	Glu	Asn	Ala	Gln	Leu	Glu	Trp	Glu	Leu	Gln	Ala	Leu	Glu				
Glu																acid leucine zipper										
1200	1205	1210	1215	1220	1225	1230	1235	1240	1245	1250	1255	1260	1265	1270	1275											
NAG	GAA	CTG	GCT	CAG	CCA	TCT	GAG	CCC	ACA	CCC	ACA	ATC	ANG	CCC	TCT	CTT	CTT	CCA	TCC	AAA	TCC	CCA	GCA	CCT		
TTC	CTT	GAC	CGA	GTC	CGT	AGA	CTC	CCG	TCT	CCC	CCG	TGT	TAG	TTC	GGG	ACA	CGA	CGT	ACG	TTC	ACG	GGT	CGT	GGA		
Lys	Glu	Leu	Ala	Gln	Ala	Ser	Glu	Pro	Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys	Pro	Cys	Lys	Cys	Pro	Ala	Pro			
1280	1285	1290	1295	1300	1305	1310	1315	1320	1325	1330	1335	1340	1345	1350												
ANAC	CTC	TTC	GGT	CGA	CCA	TCC	GTC	TTC	ATC	TTC	CCT	CCA	AAG	ATC	ANG	GAN	GTA	CTC	ATC	ATC	TCC	CTG	AGC	CCC	ATA	
TTC	GAG	ATC	CCA	CGT	CGT	ACG	CAG	ATC	TAG	ATC	ANG	CGA	GGT	TTC	TAG	TTC	CTA	CAT	GAG	TAC	TAG	AGG	GAC	TGG	GGG	TAT
Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile	Ser	Leu	Ser	Pro	Ile	
1355	1360	1365	1370	1375	1380	1385	1390	1395	1400	1405	1410	1415	1420	1425	1430											
CTC	ACA	TGT	GTC	GTC	GAT	GAT	AGC	GAG	CAT	GAC	CCA	GAT	GTC	CAG	ATC	AGC	TCC	TTC	GTC	ATC	ATC	ATC	ATC	ATC	ATC	
CAG	TGT	ACA	CAC	CAC	CTA	CAC	TCC	CTA	CTA	CTG	CGT	CTA	CAG	GTC	TAG	TCC	ACC	AAA	CAC	TTC	TTC	CAC	CTT	CAT		
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp	Pro	Asp	Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	Val	Glu	Val		
1435	1440	1445	1450	1455	1460	1465	1470	1475	1480	1485	1490	1495	1500	1505	1510											
CAC	ACA	CTT	CAG	ACA	CAA	ACC	CAT	ACA	CAG	CAT	TAC	ATC	AGT	ACT	CTC	CTT	CTG	GTC	ATC	ATC	ATC	ATC	ATC	ATC	ATC	
GTC	TGT	CGA	GTC	TGT	GTT	TCC	GTA	TCT	CTC	CTA	ATC	TTC	TCA	TCA	GAG	CCC	CAC	CAG	TCA	CCG	GAG	CCG	TAG	GTC	GTC	
Ile	Thr	Ala	Gln	Thr	Gln	Thr	Gln	Thr	His	Arg	Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg	Val	Ser	Ala	Leu	Pro	Ile	Gln	Ile

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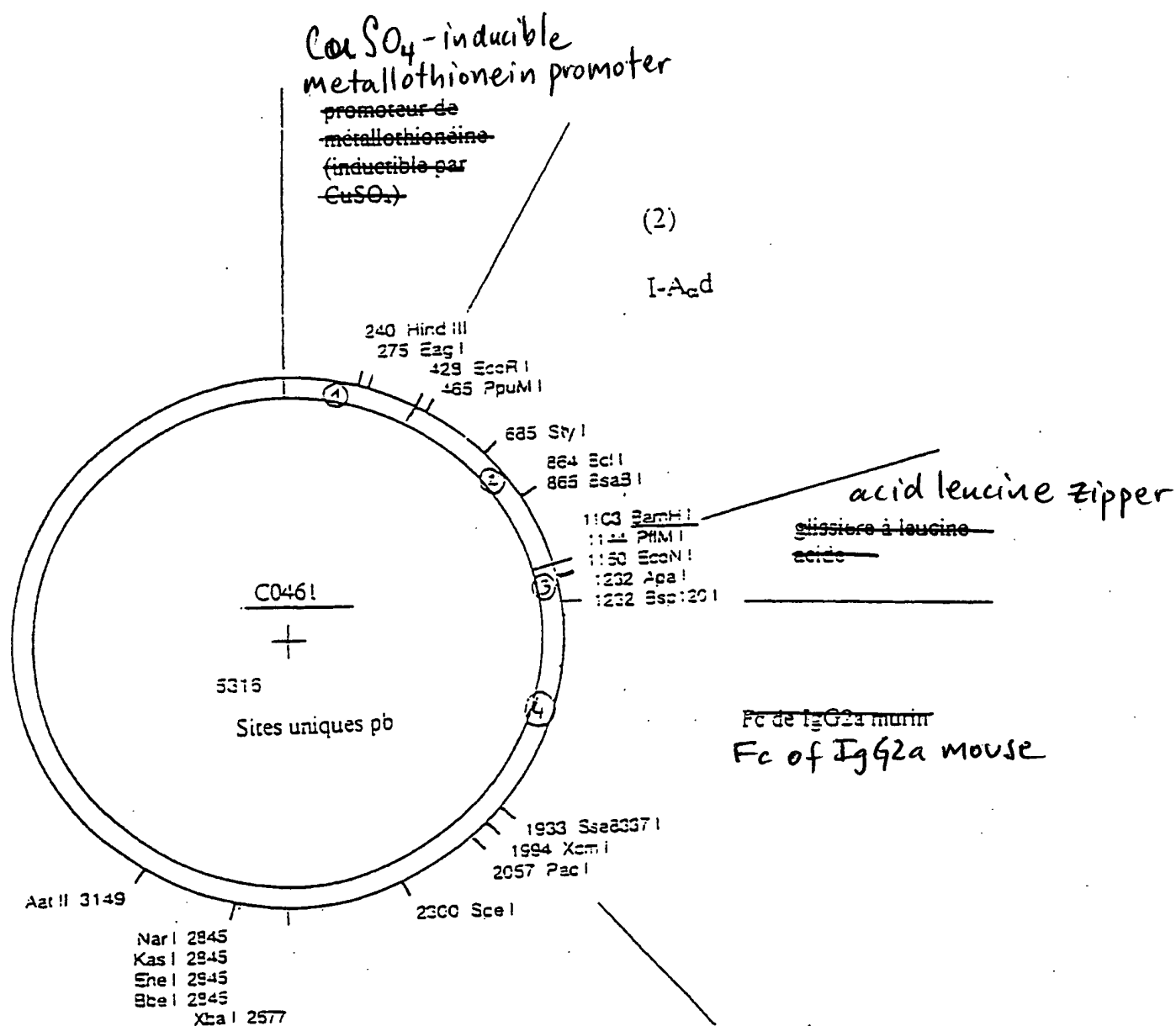
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1515 1520 1525 1530 1535 1540 1545 1550 1555 1560 1565 1570 1575 1580 1585
 CAG GAC TGG ATG AGT GGC AAG GAG TAC AAA TGC AAG GTC AAC TAC TAC TAC TAC TAC
 GTC CAG ACC TAC TCA CCG TAC CAG TAC TAC TAC TAC TAC TAC TAC TAC TAC TAC
 Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile>
 1590 1595 1600 1605 1610 1615 1620 1625 1630 1635 1640 1645 1650 1655 1660 1665
 TCA AAA CCC AAA GGG TCA GVA AGA GCT CCA CAG GVA TAT GTC TAT CCA CCA GAA GAA GAG ATG ACT AAG AAA CAG
 AGT TAT GGG TAT CCC AGT CAT TAT CGA GGT GTC CAT ATA CAG MAC GGA GGT CTT CTT CTT CTT CTT CTT CTT CTT CTT
 Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Met Thr Lys Lys Lys Gln>
 1670 1675 1680 1685 1690 1695 1700 1705 1710 1715 1720 1725 1730 1735 1740
 GTC ACT CAG ACC TGC ATG GTC ACA GAC TAT ATG CTT GAA GAC ATT TAC GTC GAG TGC ACC AAC AAC GGG AAA ACA GAG
 CAG TGA GAC TGG ACG TAC CAG TAT CAG TAT CAG TAT CAG TAT CAG TAT CAG TAT CAG TAT CAG TAT CAG TAT CAG TAT
 Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu>
 1745 1750 1755 1760 1765 1770 1775 1780 1785 1790 1795 1800 1805 1810 1815 1820
 CTA AAC TAC AAG AAC ACT GAA CCA GTC CAG TAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT
 GAT TAT AAT TAT
 Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys>
 1825 1830 1835 1840 1845 1850 1855 1860 1865 1870 1875 1880 1885 1890 1895 1900
 AAG AAC TGG GTC GAA AAT AGC TAC TAC TAT TAT TAT TAT TAT TAT TAT TAT TAT TAT TAT TAT TAT TAT TAT TAT
 TAT TAT ACC CAC CTT TAT
 Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser>
 1905 1910 1915 1920 1925 1930 1935
 TAT TAT CCG ACT CCG GGT AAA TCA TG ACT CCA CTT G
 AAG AGG GCC TGA GGC CCA TAT ACT AC TCA CTT CCA C
 Phe Ser Arg Thr Pro Gly Lys >>>>

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FIGURE 2





965 970 975 980 985 990 995 1000 1005 1010 1015 1020 1025 1030 1035 1040
 ACT CTG GTC TGT TCG GTG ACA GAT TTT TAC CCA CCC AAG ATC AAA GTC CCG TGC TTT AGG AAT GCC CAG GAG ACA
 Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala Iys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Thr>
 1045 1050 1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120
 GTC CCG GTC TCA TCC ACA CAG CTT ATT AGG AAT CCG GAC TCG ACC TTT CAG GTC CTG GTC ATG CTG GAG ATG ACC CTT
 Val Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro>
 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195
 CMT CAG CGA CAG GTC TAC ACC TGC CMT CTG CAG CMT CCC AGC CTT CAG AGC CCC ATC ACT GTG GAG TCG AGG GCA CAG
 His Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg Ala Gln>
 1200 1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270 1275
 TCC GAG TGT CCC CCG ACC AAG CGA GGT GCA TCA TCC ACT ACA GGT CCA TCA CTT CAG TTT CAG AAA TTT CAA CCA
 Ser Glu Ser Ala Arg Ser Lys Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln Leu Lys Lys Lys Leu Gln Ala>
 1280 1285 1290 1295 1300 1305 1310 1315 1320 1325 1330 1335 1340 1345 1350
 CTG AAG AAA AAG AAG CTT CAG CTT CAG TAC AAG TAC AAG CTT CAA CCC CTT CAG AAG AAA CTT GCC CAG CMT CMT CMT CMT
 Leu Lys Lys Lys Lys Asn Ala Gln Leu Lys Trp Lys Lys Lys Lys Lys Leu Ala Gln His His His His His
 1355 1360 1365 1370
 CMT TGA GT CCA CTT CC
 His >>>> Salt
 basic leucine zipper
 Histone H1

FIGURE 4

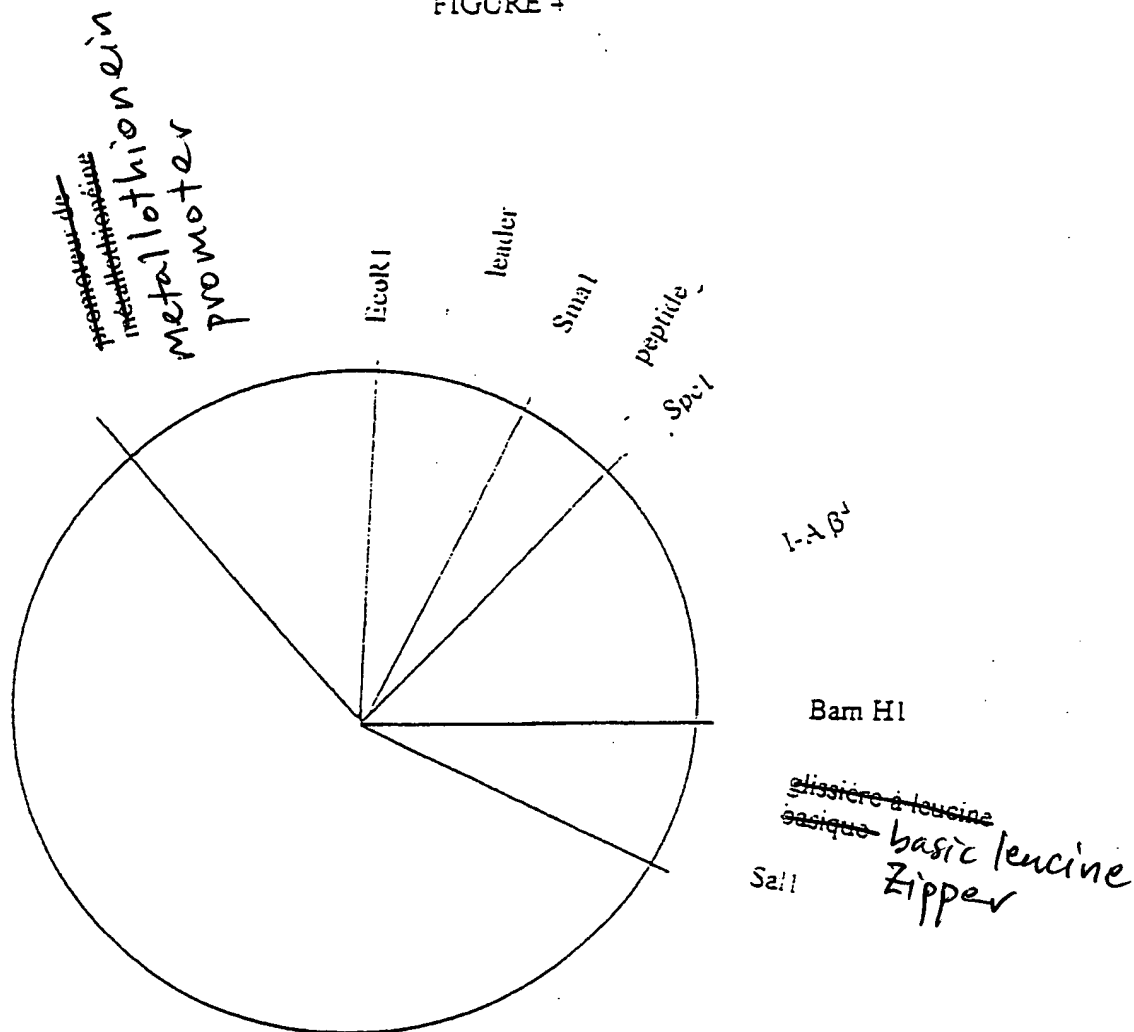


FIGURE 5

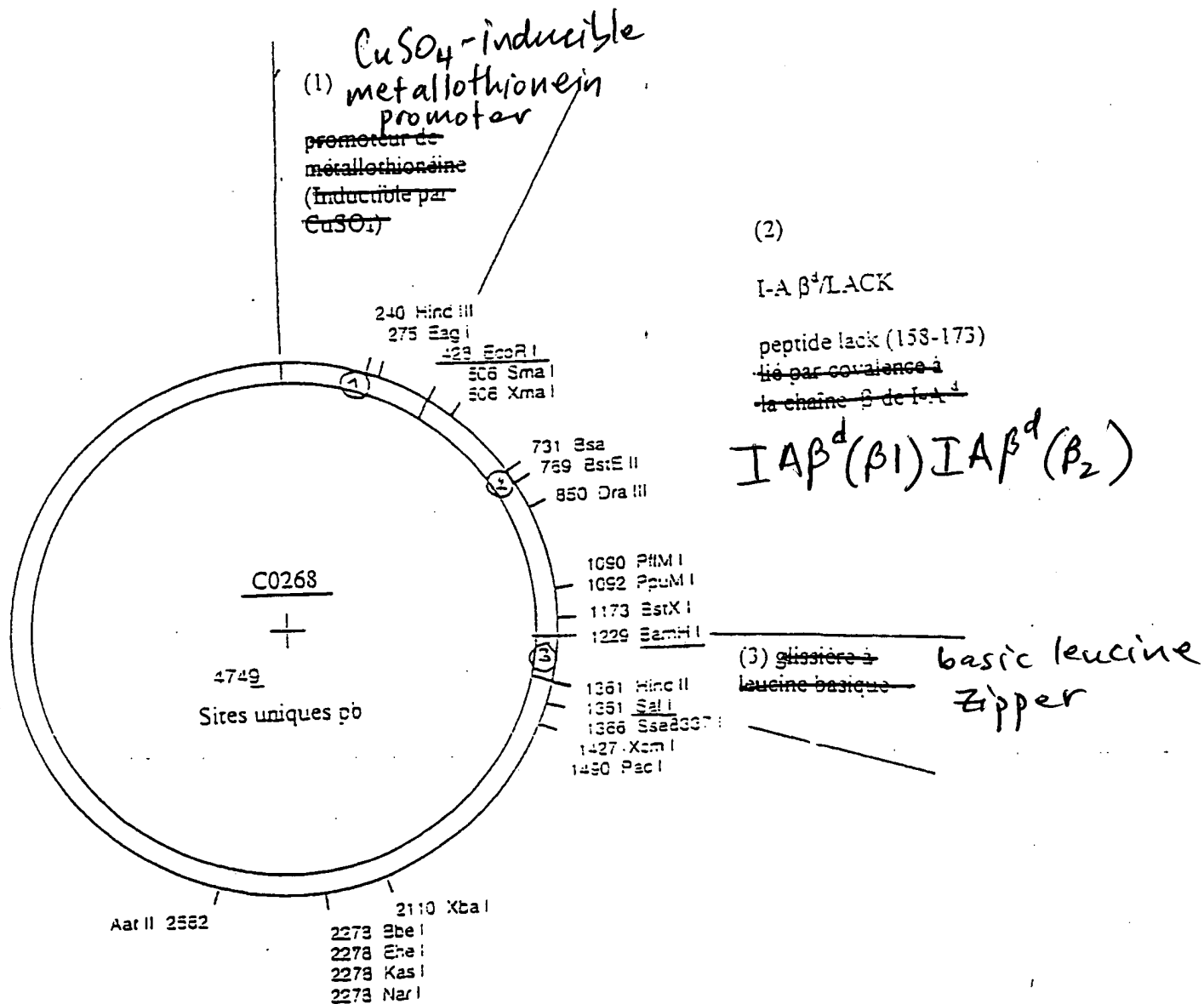


FIGURE 6

